

Gene	GenBank accession No.	Seq. ID No.	Primer	Sequence	bp position in cDNA	length (bp)
ACTB	X00351	1	Forward 5'	GAT TCC TAT GTG GGC GAC GAG 3'	192-212	
		2	Reverse 5'	CCA TCT CTT GCT CGA AGT CC 3'	704-723	532
		3	CT	5' CCA TCT CTT GCT CGA AGT CCG CCA GCC AGG TCC AGA CGC A 3'	568-587	416
ABCC1	L05628	4	Forward 5'	CAC CTG AAG GAC TTC GTG TCA G 3'	4415-4436	
		5	Reverse 5'	TGG TTT ACC AGG GGT ACT GAC T 3'	4853-4874	460
		6	CT	5' TGG TTT ACC AGG GGT ACT GAC TTT GGC CAT GCT GTA GAA AAG AC 3'	4752-4773	381
ABCC4	AF071202	7	Forward 5'	GAA GCA CCT TGG GAA TAT CAG AAA 3'	3179-3202	
		8	Reverse 5'	AGG CAC ACC AGT TGT CTT TGT CCA 3'	3652-3675	497
		9	CT	5' AGG CAC ACC AGT TGT CTT TGT CCA GTA CCT CTT GTA AGG CAT TCC ACA 3'	3552-3575	421
ABCC5	U83661	10	Forward 5'	CAT CTC TTA TGC TGT CCA GTT AAC 3'	3515-3538	
		11	Reverse 5'	GCT CTT GAG GAA TGA TAG AGA GTT 3'	3925-3948	434
		12	CT	5' GCT CTT GAG GAA TGA TAG AGA GTT GGC CAT CCC CAG CGA GGA CTT CC 3'	3814-3837	346
ABCC10	U66684	13	Forward 5'	GGA ATN GGT GAA CTG GGT GAA G 3'	1197-1218	
		14	Reverse 5'	CAA GGA GTG ATT TCC AAA GAG T 3'	1696-1717	521
		15	CT	5' CAA GGA GTG ATT TCC AAA GAG TCA GCC AGC ACC TCT GTA TAG GC 3'	1605-1626	452
DDIT3	S40706	16	Forward 5'	AGA ATC AAA AAT CTT CAC CAC T 3'	312-333	
		17	Reverse 5'	CTT TCC TTT TGT CTA CTC CAA G 3'	805-826	515
		18	CT	5' CTT TCC TTT TGT CTA CTC CAA GTC AGT AGC CAC TTC TGG GAA AG 3'	725-746	457
ERCC2	X52221/X52470	19	Forward 5'	GGC CTT CTT CAC CAG CTA C 3'	2289-2307	
		20	Reverse 5'	GTA GTC CGT CTT GCC CCT G 3'	2685-2703	415
		21	CT	5' GTA GTC CGT CTT GCC CCT GTG GAA CTG GTC CCG CAG GT 3'	2597-2615	346

Fig. 1a- Table 1

ERCC3	M31899	22 Forward	5' TCG GGG GTC ATT GTT CTT CC 3'	1098-1117
		23 Reverse	5' TCT TGG CTG GTA TGG TGT GC 3'	1424-1443
		24 CT	5' TCT TGG CTG GTA TGG TGT GCA GGT GCT AAT GGC AAC GGA G 3'	1304-1323
				246
GTF2H2	AF078847	25 Forward	5' CTC TTT CAG CAT GGC GCA TTT GGA TGG C 3'	1002-1029
		26 Reverse	5' CTT TCA ATT CCC CCT GAC ATC CAT AAC A 3'	1228-1255
		27 CT	5' CTT TCA ATT CCC CCT GAC ATC CAT AAC AGC AGA CAC CAA AGT AAG ACC AC 3'	1118-1145
				166
LIG1	M36067	28 Forward	5' CAT GAT CCT GAA GCA GAC GT 3'	1620-1639
		29 Reverse	5' GTG TCC AGG ATG AAG GAT GT 3'	1960-1979
		30 CT	5' GTG TCC AGG ATG AAG GAT GTC AGT GTT GTC TTC CTG ATT C 3'	1887-1906
				360
				307
XPA	D14533	31 Forward	5' CTC GGC GAC GGC GGC TGC GGC TAC TGG AG 3'	170-198
		32 Reverse	5' TGT CGG ACT TCC TTT GCT TCT TCT AAT GC 3'	621-649
		33 CT	5' TGT CGG ACT TCC TTT GCT TCT TCT AAT GCT CTT CAC AAT AAA TTT AAG AG 3'	508-536
				480
				391
XPC	D21089	34 Forward	5' GGC TAC TCC CAT CCC GTG ACT 3'	2509-2529
		35 Reverse	5' TTT CCC TTT TGG TCT TCT TGG 3'	2864-2884
		36 CT	5' TTT CCC TTT TGG TCT TCT TGG TCC CCT CCT CTT CAT CAG AAG 3'	2753-2773
				376
				286
XRCC1	M36089	37 Forward	5' CCC CTG AAG AGA CCA AAG CA 3'	1906-1925
		38 Reverse	5' CCA TTG AAG GCT GTG ACG TA 3'	2241-2260
		39 CT	5' CCA TTG AAG GCT GTG ACG TAT CAG GGA CTG GCA GAT CAG G 3'	2142-2161
				355
				276

Fig. 1b- Table 1 (cont.)

Fig. 2 – Table 2

	NSCLC cell line	Cisplatin
Group 1 ^b	NCI-H460	0.52 ± 0.04
	NCI-H1155	0.90 ± 0.20
	NCI-H23	2.09 ± 0.32
	NCI-H838	3.86 ± 0.31
	NCI-H1334	5.15 ± 0.47
	NCI-H1437	5.90 ± 1.61
	NCI-H1355	6.74 ± 1.29
	NCI-H1435	22.86 ± 2.36
Group 2 ^c	NCI-H358	1.16 ± 0.24
	NCI-H322	2.85 ± 0.22
	NCI-H441	3.38 ± 0.99
	NCI-H522	3.53 ± 0.56
	NCI-H226	5.05 ± 0.95
	NCI-H647	7.27 ± 1.14

^a Previously published results by Chun-Ming Tsai, et.al. (21)

^b Initial set of 8 NSCLC cell lines evaluated.

^c Additional set of 6 NSCLC cell lines evaluated.

NSCLC cell line		LIG1	ERCC2	ERCC3	DDIT3	ABCC1	ABCC4
NCI-H460	Mean	3.53E+02	2.54E+02	3.07E+02	1.00E+02	7.37E+02	3.50E+02
	S or R ^a	2.12E+01 S	2.11E+01 S	1.18E+02 S	5.26E+01 S	2.75E+02 S	2.19E+02 S
NCI-H1155	Mean	5.90E+02	5.81E+02	1.27E+03	1.26E+03	3.84E+02	3.30E+02
	S or R	7.40E+01 R	7.90E+01 R	4.70E+02 R	9.00E+01 R	1.85E+02 R	1.43E+02 R
NCI-H23	Mean	7.74E+02	8.29E+02	1.81E+03	1.55E+03	3.13E+02	1.87E+03
	S or R	2.85E+02 S	5.46E+02 S	2.47E+02 S	3.03E+02 S	9.75E+01 S	3.80E+02 S
NCI-H838	Mean	1.16E+03	8.69E+03	1.81E+03	5.79E+02	6.21E+03	1.35E+03
	S or R	5.32E+02 S	8.37E+03 R	1.35E+03 R	6.80E+02 R	3.90E+03 R	1.26E+03 R
NCI-H1334	Mean	4.50E+02	1.28E+03	7.66E+02	6.17E+02	5.48E+02	6.05E+02
	S or R	2.59E+02 S	2.12E+02 S	1.65E+02 S	1.52E+02 S	2.50E+02 S	1.12E+02 S
NCI-H1437	Mean	2.56E+02	6.13E+02	3.72E+02	4.59E+02	8.48E+02	4.05E+01
	S or R	1.42E+02 S	1.49E+02 S	7.62E+01 S	2.87E+02 S	2.71E+02 S	3.37E+01 S
NCI-H1355	Mean	9.03E+02	6.52E+02	1.01E+03	3.75E+02	1.48E+03	1.10E+03
	S or R	4.45E+02 S	2.57E+02 S	3.36E+02 S	2.49E+02 S	4.72E+02 S	1.80E+02 S
NCI-H1435	Mean	2.59E+03	3.01E+04	3.37E+03	3.76E+03	9.24E+03	2.24E+03
	S or R	7.47E+02 S	8.82E+03 S	1.14E+03 S	1.40E+03 S	3.71E+03 S	8.75E+02 S
NCI-H358	Mean	1.32E+03					
	S or R	4.40E+02 S					
NCI-H322	Mean	4.02E+03					
	S or R	1.58E+03 S					
NCI-H441	Mean	1.19E+03					
	S or R	2.52E+02 S					
NCI-H522	Mean	7.12E+02					
	S or R	1.62E+02 S					
NCI-H226	Mean	8.85E+02					
	S or R	2.74E+02 S					
NCI-H647	Mean	4.64E+03					
	S or R	2.84E+03 S					

Fig. 3a – Table 3

NSCLC cell line		ABCC5	ABCC10	GTF2H2	XPA	XPC	XRCC1
NCI-H460	Mean	5.93E+01	1.80E+01	1.02E+03	3.10E+02	5.25E+02	1.88E+03
	S or R ^a	2.61E+01 S	2.65E+00 S	3.58E+02 S	2.53E+02 S	1.74E+02 S	7.60E+02 S
NCI-H1155	Mean	8.97E+01	4.25E+01	1.09E+03	1.65E+03	2.33E+03	4.04E+03
	S or R	3.23E+01 S	3.70E+01 R	7.47E+02 R	1.75E+03 R	6.50E+02 R	1.60E+02 R
NCI-H23	Mean	1.39E+02	4.56E+02	4.42E+03	1.18E+03	1.44E+03	8.27E+03
	S or R	1.50E+01 S	2.62E+02 S	3.24E+03 S	2.53E+02 S	7.98E+02 S	6.52E+03 S
NCI-H838	Mean	4.01E+02	5.12E+02	4.18E+03	2.23E+03	5.35E+03	3.14E+04
	S or R	5.90E+01 R	3.30E+02 R	2.73E+03 R	2.16E+03 R	6.05E+03 R	3.75E+04 R
NCI-H1334	Mean	9.90E+01	1.17E+02	1.33E+03	5.07E+02	1.18E+03	6.53E+03
	S or R	4.51E+01 S	6.17E+01 S	4.46E+02 S	3.91E+02 S	1.50E+02 S	1.93E+03 S
NCI-H1437	Mean	2.64E+02	2.00E+02	1.74E+03	5.84E+02	7.30E+02	2.84E+03
	S or R	2.02E+02 S	2.08E+02 S	5.20E+02 S	2.98E+02 S	5.79E+02 S	6.49E+02 S
NCI-H1355	Mean	2.67E+02	8.28E+01	1.04E+03	1.34E+03	1.37E+03	4.57E+03
	S or R	2.47E+02 S	4.12E+01 S	4.73E+02 S	5.10E+02 S	7.70E+02 S	7.38E+02 S
NCI-H1435	Mean	1.39E+03	3.31E+02	2.84E+03	6.77E+03	1.93E+03	4.19E+04
	S or R	6.10E+02 S	8.14E+01 S	3.84E+02 S	1.79E+03 S	5.38E+02 S	2.87E+03 S
NCI-H358	Mean	6.80E+01		1.02E+03	1.34E+03	1.03E+03	4.02E+03
	S or R	3.10E+01 S		6.73E+02 S	6.63E+02 S	3.18E+02 S	1.72E+03 S
NCI-H322	Mean	4.50E+01		6.63E+02	6.64E+02	5.51E+02	3.87E+03
	S or R	8.00E+00 S		1.22E+02 S	3.42E+02 S	3.14E+02 S	7.91E+02 S
NCI-H441	Mean	1.57E+02		1.14E+03	6.11E+02	7.28E+02	2.96E+03
	S or R	5.50E+01 S		3.23E+02 S	1.32E+02 S	1.46E+02 S	6.11E+02 S
NCI-H522	Mean	4.03E+02		2.46E+03	4.83E+02	4.54E+02	2.41E+03
	S or R	4.00E+01 S		1.43E+03 S	2.68E+02 S	3.00E+01 S	5.82E+02 S
NCI-H226	Mean	1.04E+02		1.10E+03	5.97E+02	3.52E+03	2.46E+03
	S or R	1.60E+01 S		3.85E+02 S	1.17E+02 S	1.31E+03 S	7.94E+02 S
NCI-H647	Mean	1.92E+02		8.84E+02	1.06E+03	2.71E+03	1.04E+04
	S or R	3.90E+01 S		1.22E+02 S	4.90E+02 S	8.06E+02 S	4.94E+03 S

Fig. 3b – Table 3 (cont.)

Gene	Group 1 ^a		Groups 1 and 2 ^b	
	R ²	p value	R ²	p value
ABCC5	0.93	0.0001	0.85	0.0001
ERCC2	0.85	0.0012	0.82	0.0001
XPA	0.81	0.0023	0.75	0.0001
LIG1	0.78	0.0034	Nac	
DDIT3	0.68	0.0120	NA	
ABCC1	0.64	0.0164	NA	
XRCC1	0.56	0.0318	0.57	0.0019
ERCC3	0.56	0.0319	NA	
ABCC4	0.37	0.1081	NA	
ABCC10	0.06	0.5641	NA	
GTF2H2	0.02	0.7424	0.04	0.5183
XPC	0.00	0.9851	0.02	0.6654

^a Initial 8 NSCLC cell lines analyzed as reported in Table 2.

^b All 14 NSCLC cell lines analyzed as reported in Table 2.

^c Not assessed.

Fig. 4 - Table 4

Model	Group 1 ^b		Groups 1 and 2 ^c	
	Model R ²	p value ^d	Model R ²	p value
Single variable				
ERCC2/XPC	0.91	0.0002	0.69	0.0002
ABCC5/GTF2H2	0.91	0.0002	0.88	0.0001
ERCC2/XRCC1	0.90	0.0003	NS ^e	
ERCC2/GTF2H2	0.90	0.0004	0.63	0.0007
XPA/XPC	0.89	0.0004	0.62	0.0008
XRCC1/XPC	0.88	0.0005	0.75	0.0001
ABCC5/XPC	0.88	0.0006	0.29	0.0461
Two variable				
ABCC5/GTF2H2 and ERCC2/GTF2H2	0.96	0.0003	0.91	0.0001

^a SAS version 6, 4th edition, volume 2.

^b 8 NSCLC cell lines analyzed as reported in Table 2.

^c 14 NSCLC cell lines analyzed as reported in Table 2.

^d p value is shown for each ratio in the model.

^e not significant (p > 0.05).

Fig. 5 - Table 5

Effect of Collection Methods on RNA Quality in H1155 Human NSCLC Cells

Collection agent	1 day RNA	3 day RNA	actin	10 day RNA	actin	30 day RNA	actin
Preservcyt-4	^a ++	++	^b +NT	++	+NT	++	+NT
Preservcyt-20	++	++	+NT	++	+NT	++	+NT
RNA Later-4	++	++	+NT	++	+NT	+	+NT
RNA Later-20	++	++	+NT	++	+NT	-	^c -NT
Tri-reagent-4	++	++	+NT	++	+NT	++	+NT
Tri-reagent-20	++	++	+NT	++	+NT	++	+NT

^a ++ = 2 ribosomal peaks; ^b +NT = native actin; ^c -NT = no native actin

Fig. 6 – Table 6

Cytological Information and Diagnosis of FNA specimens

FNA Sample	Cellularit	% Tumor	Viability	FNA Diagnosis	Final Diagnosis	RNA Quality	β-actin
110	Y	90	H	NSCLC	Squamous	+-	+
123	L	90	L	NSCLC	Squamous	++	+
125	H	90	H	NSCLC	NSCLC	++	+
135	L	70	L	NSCLC	NSCLC	--	-
138	H	90	I	NSCLC	NSCLC	NE	+
148a	L	80	L	Atypical	SCLC	++	+
148b	L	60	L	Atypical	SCLC	--	+
165	L	20	L	Atypical	SCLC	+-	+
171	L	10	L	Atypical	NSCLC	--	-
172	L	20	L	NSCLC	NSCLC	--	+

Fig. 7 – Table 7

10/508932

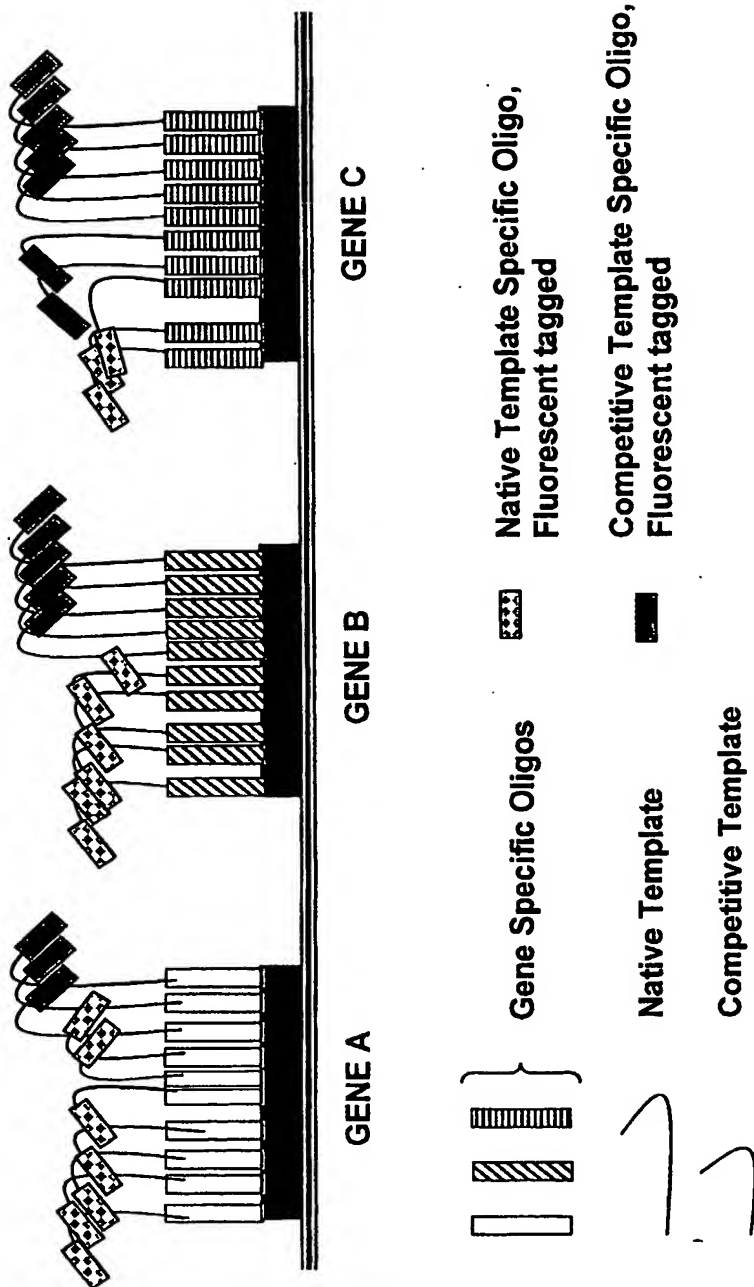
Gene Expression Values and Index Value for c-myc, E2F-1 and p21 in FNA samples

Sample		c-myc	E2F-1	p21	Index
110	Mean	2.51E+05	4.85E+03	1.13E+05	1.00E+04
	S.D.	3.80E+05	4.60E+03	3.90E+04	
123	Mean	3.25E+05	5.49E+04	9.00E+04	2.00E+05
	S.D.	4.50E+04	2.30E+04	4.10E+04	
125	Mean	1.24E+05	4.08E+04	1.13E+05	4.50E+04
	S.D.	1.30E+05	1.80E+04	3.20E+04	
138	Mean	8.69E+04	2.30E+04	2.08E+04	9.70E+04
	S.D.	4.10E+04	3.40E+03	6.90E+03	
148a	Mean	1.87E+03	1.82E+05	4.84E+04	7.00E+03
	S.D.	1.10E+03	2.50E+04	2.50E+04	
148b	Mean	1.32E+03	3.48E+06	7.32E+04	6.30E+04
	S.D.	2.00E+02	4.70E+05	1.10E+04	
165	Mean	1.64E+04	3.59E+04	8.98E+03	2.00E+04
	S.D.	6.50E+03	1.90E+04	9.50E+02	
172	Mean	2.88E+06	1.72E+05	1.44E+05	3.40E+06
	S.D.	7.50E+05	3.30E+04	1.20E+05	

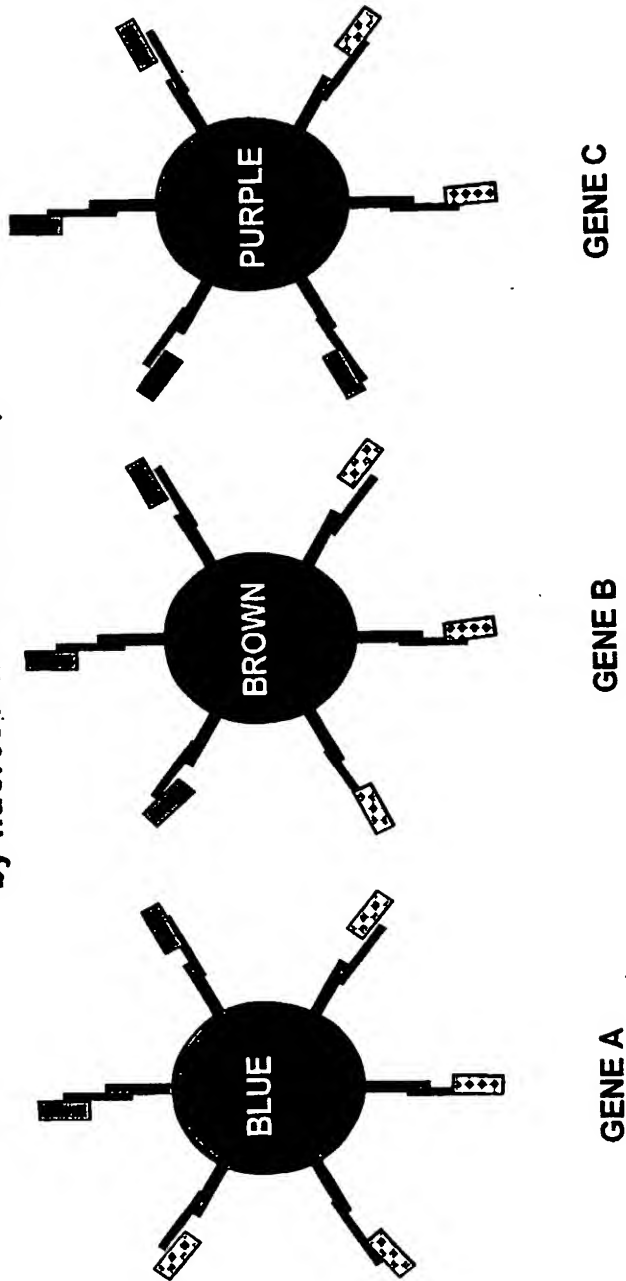
*No data obtained for sample 135 and 171.

Fig. 8 – Table 8

Fig. 9a MICROARRAYS (Identity of gene known
by location on microarray)



**Fig. 9b MICROBEADS (Identity of gene known
by fluorescent color of bead)**



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